RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 09/910,208B
Source: IFW16
Date Processed by STIC: 12/22/04

ENTERED

IFW16

RAW SEQUENCE LISTING DATE: 12/22/2004
PATENT APPLICATION: **US/09/910,208B** TIME: 16:46:26

Input Set : **N:\AMC\I910208b.raw**
Output Set: **N:\CRF4\12222004\I910208B.raw**

```
      1 <110> APPLICANT: Hitomi, Jiro
      2       Yamamura, Tokujiro
      3       Kimura, Tatsuji
      4       Yamaguchi, Ken
      5 <120> TITLE OF INVENTION: Novel Calcium-Binding Proteins
      6 <130> FILE REFERENCE: MM4454
C-->  7 <140> CURRENT APPLICATION NUMBER: US/09/910,208B
      8 <141> CURRENT FILING DATE: 2001-07-20
      9 <160> NUMBER OF SEQ ID NOS: 18
     10 <170> SOFTWARE: PatentIn version 3.2
     12 <210> SEQ ID NO: 1
     13 <211> LENGTH: 429
     14 <212> TYPE: DNA
     15 <213> ORGANISM: calcium-binding protein
     16 <220> FEATURE:
     17 <221> NAME/KEY: exon
     18 <222> LOCATION: (48)..(323)
     19 <223> OTHER INFORMATION: Amino acid sequence of calcium-binding protein from bovine
     20       amniotic fluid
     21 <400> SEQUENCE: 1
     22       ctggcattcc acacttctgt gcagaggggt gaacgtagtt tggtaaa atg act aag       56
     23                                                        Met Thr Lys
     24                                                        1
     25       ctg gaa gat cac ctg gag gga atc atc aac atc ttc cac cag tac tcc      104
     26       Leu Glu Asp His Leu Glu Gly Ile Ile Asn Ile Phe His Gln Tyr Ser
     27           5                   10                  15
     28       gtt cgg gtg ggg cat ttc gac acc ctc aac aag cgt gag ctg aag cag      152
     29       Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu Lys Gln
     30       20                  25                  30                  35
     31       ctg atc aca aag gaa ctt ccc aaa acc ctc cag aac acc aaa gat caa      200
     32       Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln
     33                       40                  45                  50
     34       cct acc att gac aaa ata ttc caa gac ctg gat gcc gat aaa gac gga      248
     35       Pro Thr Ile Asp Lys Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly
     36                   55                  60                  65
     37       gcc gtc agc ttt gag gaa ttc gta gtc ctg gtg tcc agg gtg ctg aaa      296
     38       Ala Val Ser Phe Glu Glu Phe Val Val Leu Val Ser Arg Val Leu Lys
     39               70                  75                  80
     40       aca gcc cac ata gat atc cac aaa gag taggaagctc tttccagcaa            343
     41       Thr Ala His Ile Asp Ile His Lys Glu
     42           85                  90
     43       tgtccccaag aagacttacc cttctcctcc ctgaggctgc cttacccgag ggaagagaga    403
     44       attaataaac gtactttggc aaagtt                                        429
```

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Input Set : **N:\AMC\I910208b.raw**
Output Set: **N:\CRF4\12222004\I910208B.raw**

```
<210> SEQ ID NO: 2
<211> LENGTH: 50
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 2
      Thr Lys Leu Glu His Leu Glu Gly Ile Ile Asn Ile Phe His Gln Tyr
      1               5                   10                  15
      Ser Val Arg Val Gly His Phe Asp Thr Leu Asn Lys Arg Glu Leu Lys
                  20                  25                  30
      Gln Leu Ile Thr Lys Glu Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp
              35                  40                  45
      Gln Pro
          50
<210> SEQ ID NO: 3
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 3
      Ile Phe Gln Asp Leu Asp Ala Asp
      1               5
<210> SEQ ID NO: 4
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 4
      Asp Gly Ala Val Ser Phe Glu Glu Phe Val Val Leu
      1               5                   10
<210> SEQ ID NO: 5
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 5
      Thr Ala His Ile Asp Ile His Lys Glu
      1               5
<210> SEQ ID NO: 6
<211> LENGTH: 31
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 6
      Leu Pro Lys Thr Leu Gln Asn Thr Lys Asp Gln Pro Thr Ile Asp Lys
      1               5                   10                  15
      Ile Phe Gln Asp Leu Asp Ala Asp Lys Asp Gly Ala Val Ser Phe
                  20                  25                  30
<210> SEQ ID NO: 7
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Bos taurus
<400> SEQUENCE: 7
      Glu Phe Val Val Leu Val Ser Arg Val Leu Lys Arg Ala His Ile Asp
```

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Input Set : **N:\AMC\I910208b.raw**
Output Set: **N:\CRF4\12222004\I910208B.raw**

100 1 5 10 15
101 Ile His Lys Glu
102 20
104 <210> SEQ ID NO: 8
105 <211> LENGTH: 20
106 <212> TYPE: DNA
107 <213> ORGANISM: artificial
108 <220> FEATURE:
109 <223> OTHER INFORMATION: sense primer
110 <220> FEATURE:
111 <221> NAME/KEY: misc_feature
112 <222> LOCATION: (3)..(3)
113 <223> OTHER INFORMATION: n is a, c, g, or t
114 <220> FEATURE:
115 <221> NAME/KEY: misc_feature
116 <222> LOCATION: (15)..(15)
117 <223> OTHER INFORMATION: n is a, c, g, or t
118 <400> SEQUENCE: 8
W--> 119 **ttngargayc ayytngargg** 20
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 20
123 <212> TYPE: DNA
124 <213> ORGANISM: artificial
125 <220> FEATURE:
126 <223> OTHER INFORMATION: antisense primer
127 <220> FEATURE:
128 <221> NAME/KEY: misc_feature
129 <222> LOCATION: (18)..(18)
130 <223> OTHER INFORMATION: n is a, c, g, or t
131 <400> SEQUENCE: 9
W--> 132 **ttrtgdatrt cdatrtgngc** 20
134 <210> SEQ ID NO: 10
135 <211> LENGTH: 23
136 <212> TYPE: DNA
137 <213> ORGANISM: artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: forward primer
140 <400> SEQUENCE: 10
141 ggtggcacga ctcctggagc ccg 23
143 <210> SEQ ID NO: 11
144 <211> LENGTH: 24
145 <212> TYPE: DNA
146 <213> ORGANISM: artificial
147 <220> FEATURE:
148 <223> OTHER INFORMATION: reverse primer
149 <400> SEQUENCE: 11
150 ttgacaccag accaactggt aatg 24
152 <210> SEQ ID NO: 12
153 <211> LENGTH: 440

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Input Set : **N:\AMC\I910208b.raw**
Output Set: **N:\CRF4\12222004\I910208B.raw**

```
154 <212> TYPE: DNA
155 <213> ORGANISM: humab calcium-binding protein
156 <220> FEATURE:
157 <221> NAME/KEY: exon
158 <222> LOCATION: (22)..(297)
159 <223> OTHER INFORMATION: Deduced amino acid sequence for human calcium-binding
protein.
160 <400> SEQUENCE: 12
161       ggttaacatt aggctgggaa g atg aca aaa ctt gaa gag cat ctg gag gga       51
162                               Met Thr Lys Leu Glu Glu His Leu Glu Gly
163                               1               5                   10
164       att gtc aat atc ttc cac caa tac tca gtt cgg aag ggg cat ttt gac       99
165       Ile Val Asn Ile Phe His Gln Tyr Ser Val Arg Lys Gly His Phe Asp
166                       15                  20                  25
167       acc ctc tct aag ggt gag ctg aag cag ctg ctt aca aag gag ctt gca      147
168       Thr Leu Ser Lys Gly Glu Leu Lys Gln Leu Leu Thr Lys Glu Leu Ala
169                   30                  35                  40
170       aac acc atc aag aat atc aaa gat aaa gct gtc att gat gaa ata ttc      195
171       Asn Thr Ile Lys Asn Ile Lys Asp Lys Ala Val Ile Asp Glu Ile Phe
172               45                  50                  55
173       caa ggc ctg gat gct aat caa gat gaa cag gtc gac ttt caa gaa ttc      243
174       Gln Gly Leu Asp Ala Asn Gln Asp Glu Gln Val Asp Phe Gln Glu Phe
175           60                  65                  70
176       ata tcc ctg gta gcc att gcg ctg aag gct gcc cat tac cac acc cac      291
177       Ile Ser Leu Val Ala Ile Ala Leu Lys Ala Ala His Tyr His Thr His
178       75                  80                  85                  90
179       aaa gag taggtagctc tctgaagctt tttacccagc aatgtcctca atgagggtct      347
180       Lys Glu
181       tttctttccc tcaccaaaac ccagccttgc ccgtggggag taagagttaa taaacacact    407
182       cacgaaaagt taaaaaaaaa aaaaaaaaat tct                                 440
184 <210> SEQ ID NO: 13
185 <211> LENGTH: 20
186 <212> TYPE: DNA
187 <213> ORGANISM: artificial
188 <220> FEATURE:
189 <223> OTHER INFORMATION: sense primer
190 <400> SEQUENCE: 13
191       actatcaaca tcttccacca                                                20
193 <210> SEQ ID NO: 14
194 <211> LENGTH: 20
195 <212> TYPE: DNA
196 <213> ORGANISM: artificial
197 <220> FEATURE:
198 <223> OTHER INFORMATION: antisense primer
199 <400> SEQUENCE: 14
200       tctttatcgg catccaggtc                                                20
202 <210> SEQ ID NO: 15
203 <211> LENGTH: 15
204 <212> TYPE: DNA
205 <213> ORGANISM: artificial
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RAW SEQUENCE LISTING DATE: 12/22/2004
PATENT APPLICATION: **US/09/910,208B** TIME: 16:46:26

Input Set : **N:\AMC\I910208b.raw**
Output Set: **N:\CRF4\12222004\I910208B.raw**

206 <220> FEATURE:
207 <223> OTHER INFORMATION: primer PMN.HP7S 1-15
208 <400> SEQUENCE: 15
209 tactcagttc ggaag 15
211 <210> SEQ ID NO: 16
212 <211> LENGTH: 15
213 <212> TYPE: DNA
214 <213> ORGANISM: artificial
215 <220> FEATURE:
216 <223> OTHER INFORMATION: primer PMN.HP7A 126-112
217 <400> SEQUENCE: 16
218 ttggaatatt tcatc 15
220 <210> SEQ ID NO: 17
221 <211> LENGTH: 20
222 <212> TYPE: DNA
223 <213> ORGANISM: artificial
224 <220> FEATURE:
225 <223> OTHER INFORMATION: primer HP7S 7-26
226 <400> SEQUENCE: 17
227 acattaggct gggaagatga 20
229 <210> SEQ ID NO: 18
230 <211> LENGTH: 20
231 <212> TYPE: DNA
232 <213> ORGANISM: artificial
233 <220> FEATURE:
234 <223> OTHER INFORMATION: primer HP7A 336-317
235 <400> SEQUENCE: 18
236 ggacattgct gggtaaaaag 20

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/22/2004
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Input Set : **N:\AMC\I910208b.raw**
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 3,15
Seq#:9; N Pos. 18

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 19
Seq#:12; Line(s) 159

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,13,14,15,16,17,18

VERIFICATION SUMMARY DATE: 12/22/2004
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Input Set : **N:\AMC\I910208b.raw**
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L:7 M:270 C: Current Application Number differs, Wrong Format
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0